

1600

CRF Errors Edited by the STIC Systems Branch

Serial Number: 09/759,152A

CRF Edit Date: 10/21/83
Edited by: W

RECEIVED

OCT 27 2003

TECH CENTER 1600/2900

ENTERED

Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Deleted: invalid beginning/end-of-file text ; page numbers

Inserted mandatory headings/numeric identifiers, specifically:

Moved responses to same line as heading/numeric identifier, specifically:

Other: Sequence 10 - inserted hard returns



1600

RAW SEQUENCE LISTING

DATE: 10/21/2003

PATENT APPLICATION: US/09/759,152A

TIME: 17:58:53

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\10212003\I759152A.raw

4 <110> APPLICANT: Palmer, Michelle A.J.
 5 Gee, Melissa
 6 Tillotson, Bonnie
 7 Chang, Xiao-Jia
 9 <120> TITLE OF INVENTION: Systems for Sensitive Detection of G-Protein Coupled
 10 Receptor and Orphan Receptor Function Using Reporter
 11 Enzyme Mutant Complementation
 13 <130> FILE REFERENCE: 4085-235-27 CIP
 15 <140> CURRENT APPLICATION NUMBER: US 09/759,152A
 16 <141> CURRENT FILING DATE: 2001-01-16
 18 <150> PRIOR APPLICATION NUMBER: US 09/654,499
 19 <151> PRIOR FILING DATE: 2000-09-01
 21 <150> PRIOR APPLICATION NUMBER: US 60/180,669
 22 <151> PRIOR FILING DATE: 2000-02-07
 24 <160> NUMBER OF SEQ ID NOS: 10
 26 <170> SOFTWARE: PatentIn version 3.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 6700
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Unknown
 33 <220> FEATURE:
 34 <223> OTHER INFORMATION: pICAST ALC.
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (1457)..(4486)
 40 <400> SEQUENCE: 1
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 43 gggccaagaa cagatggaac agctgaatat gggccaaaca ggatatctgt ggtaagcagt 120
 45 tcctgccccg gctcagggcc aagaacagat ggtccccaga tgcggtccag ccctcagcag 180
 47 tttctagaga accatcagat gtttccaggg tgccccaagg acctgaaatg accctgtgcc 240
 49 ttatttgaac taaccaatca gttcgtttct cgcttctggt cgcgcgcttc tgctccccga 300
 51 gctcaataaa agagcccaca acccctcact cggggcgcca gtccctccgat tgactgagtc 360
 53 gcccggttac ccgtgtatcc aataaaccct cttgcagttg catccgactt gtggtctcgc 420
 55 tgttccttgg gaggttctcc tctgagtgat tgactaccgc tcagcggggg tctttcattt 480
 57 gggggctcgt ccgggatcgg gagaccctcg cccagggacc accgaccac caccgggagg 540
 58 caagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttta 600
 62 tgcgcctgcg tcggtactag ttagctaact agctctgtat ctggcggaacc cgtggtggaa 660
 64 ctgacgagtt ctgaacaccc ggccgcaacc ctgggagacg tcccagggaac tttgggggcc 720
 66 gtttttgtgg cccgacctga ggaagggagt cgatgtggaa tccgaccccg tcaggatatg 780
 68 tggttcttgt aggagacgag aacctaaaac agttcccgc tccgtctgaa tttttgcttt 840
 70 cggtttgtaa ccgaagccgc gcgtcttgtc tgctgcagca tcgttctgtg ttgtctctgt 900
 72 ccgactgtgt ttctgtattt gtctgaaaat tagggccaga ctgttaccac tcccttaagt 960
 74 ttgaccttag gtaactggaa agatgtcgag cggctcgctc acaaccagtc ggtagatgtc 1020

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78 cgcgagacg gcacctttaa ccgagacctc atcaccagg ttaagatcaa ggtcttttca 1140
80 cctggcccgcc atggacaccc agaccaggtc ccctacatcg tgacctggga agccttggct 1200
82 tttgaccccc ctccctgggt caagcccttt gtacacccta agcctccgcc tcctcttctt 1260
84 ccatccgccc cgtctctccc ccttgaacct cctcgttcga ccccgctcgc atcctccctt 1320
86 tatccagccc tcaactcttc tctaggcgcc ggccgctcta gccattaat acgactcact 1380
88 atagggcgat tcgaatcagg ccttggcgcg ccggatcctt aattaagcgc aattgggagg 1440
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91 Met Gly Val Ile Thr Asp Ser Leu Ala Val Val Ala
92 1 5 10
94 cgc acc gat cgc cct tcc caa cag tta cgc agc ctg aat ggc gaa tgg 1540
95 Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp
96 15 20 25
98 cgc ttt gcc tgg ttt ccg gca cca gaa gcg gtg ccg gaa agc tgg ctg 1588
99 Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu
100 30 35 40
102 gag tgc gat ctt cct gag gcc gat act gtc gtc gtc ccc tca aac tgg 1636
103 Glu Cys Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp
104 45 50 55 60
106 cag atg cac ggt tac gat gcg ccc atc tac acc aac gtg acc tat ccc 1684
107 Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro
108 65 70 75
110 att acg gtc aat ccg ccg ttt gtt ccc acg gag aat ccg acg ggt tgt 1732
111 Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys
112 80 85 90
114 tac tcg ctc aca ttt aat gtt gat gaa agc tgg cta cag gaa ggc cag 1780
115 Tyr Ser Leu Thr Phe Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln
116 95 100 105
117 acg cga att att ttt gat ggc gtt aac tcg gcg ttt cat ctg tgg tgc 1828
118 Thr Arg Ile Ile Phe Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys
119 110 115 120
123 aac ggg cgc tgg gtc ggt tac ggc cag gac agt cgt ttg ccg tct gaa 1876
124 Asn Gly Arg Trp Val Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu
125 125 130 135 140
127 ttt gac ctg agc gca ttt tta cgc gcc gga gaa aac cgc ctc gcg gtg 1924
128 Phe Asp Leu Ser Ala Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val
129 145 150 155
131 atg gtg ctg cgc tgg agt gac ggc agt tat ctg gaa gat cag gat atg 1972
132 Met Val Leu Arg Trp Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met
133 160 165 170
135 tgg cgg atg agc ggc att ttc cgt gac gtc tcg ttg ctg cat aaa ccg 2020
136 Trp Arg Met Ser Gly Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro
137 175 180 185
139 act aca caa atc agc gat ttc cat gtt gcc act cgc ttt aat gat gat 2068
140 Thr Thr Gln Ile Ser Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp
141 190 195 200
143 ttc agc cgc gct gta ctg gag gct gaa gtt cag atg tgc ggc gag ttg 2116
144 Phe Ser Arg Ala Val Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu
145 205 210 215 220

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148	Arg	Asp	Tyr	Leu	Arg	Val	Thr	Val	Ser	Leu	Trp	Gln	Gly	Glu	Thr	Gln	
149				225						230					235		
151	gtc	gcc	agc	ggc	acc	gcg	cct	ttc	ggc	ggt	gaa	att	atc	gat	gag	cgt	2212
152	Val	Ala	Ser	Gly	Thr	Ala	Pro	Phe	Gly	Gly	Glu	Ile	Ile	Asp	Glu	Arg	
153				240					245					250			
155	ggt	ggt	tat	gcc	gat	cgc	gtc	aca	cta	cgt	ctg	aac	gtc	gaa	aac	ccg	2260
156	Gly	Gly	Tyr	Ala	Asp	Arg	Val	Thr	Leu	Arg	Leu	Asn	Val	Glu	Asn	Pro	
157			255					260					265				
159	aaa	ctg	tgg	agc	gcc	gaa	atc	ccg	aat	ctc	tat	cgt	gcg	gtg	gtt	gaa	2308
160	Lys	Leu	Trp	Ser	Ala	Glu	Ile	Pro	Asn	Leu	Tyr	Arg	Ala	Val	Val	Glu	
161		270						275				280					
163	ctg	cac	acc	gcc	gac	ggc	acg	ctg	att	gaa	gca	gaa	gcc	tgc	gat	gtc	2356
164	Leu	His	Thr	Ala	Asp	Gly	Thr	Leu	Ile	Glu	Ala	Glu	Ala	Cys	Asp	Val	
165	285					290				295					300		
167	ggt	ttc	cgc	gag	gtg	cgg	att	gaa	aat	ggt	ctg	ctg	ctg	ctg	aac	ggc	2404
168	Gly	Phe	Arg	Glu	Val	Arg	Ile	Glu	Asn	Gly	Leu	Leu	Leu	Leu	Asn	Gly	
169				305					310					315			
171	aag	ccg	ttg	ctg	att	cga	ggc	gtt	aac	cgt	cac	gag	cat	cat	cct	ctg	2452
172	Lys	Pro	Leu	Leu	Ile	Arg	Gly	Val	Asn	Arg	His	Glu	His	His	Pro	Leu	
173				320					325					330			
175	cat	ggt	cag	gtc	atg	gat	gag	cag	acg	atg	gtg	cag	gat	atc	ctg	ctg	2500
176	His	Gly	Gln	Val	Met	Asp	Glu	Gln	Thr	Met	Val	Gln	Asp	Ile	Leu	Leu	
177			335					340					345				
179	atg	aag	cag	aac	aac	ttt	aac	gcc	gtg	cgc	tgt	tcg	cat	tat	ccg	aac	2548
180	Met	Lys	Gln	Asn	Asn	Phe	Asn	Ala	Val	Arg	Cys	Ser	His	Tyr	Pro	Asn	
181		350					355				360						
184	cat	ccg	ctg	tgg	tac	acg	ctg	tgc	gac	cgc	tac	ggc	ctg	tat	gtg	gtg	2596
185	His	Pro	Leu	Trp	Tyr	Thr	Leu	Cys	Asp	Arg	Tyr	Gly	Leu	Tyr	Val	Val	
186	365					370				375					380		
188	gat	gaa	gcc	aat	att	gaa	acc	cac	ggc	atg	gtg	cca	atg	aat	cgt	ctg	2644
189	Asp	Glu	Ala	Asn	Ile	Glu	Thr	His	Gly	Met	Val	Pro	Met	Asn	Arg	Leu	
190				385					390					395			
192	acc	gat	gat	ccg	cgc	tgg	cta	ccg	gcg	atg	agc	gaa	cgc	gta	acg	cga	2692
193	Thr	Asp	Asp	Pro	Arg	Trp	Leu	Pro	Ala	Met	Ser	Glu	Arg	Val	Thr	Arg	
194				400					405					410			
196	atg	gtg	cag	cgc	gat	cgt	aat	cac	ccg	agt	gtg	atc	atc	tgg	tcg	ctg	2740
197	Met	Val	Gln	Arg	Asp	Arg	Asn	His	Pro	Ser	Val	Ile	Ile	Trp	Ser	Leu	
198			415					420					425				
200	ggg	aat	gaa	tca	ggc	cac	ggc	gct	aat	cac	gac	gcg	ctg	tat	cgc	tgg	2788
201	Gly	Asn	Glu	Ser	Gly	His	Gly	Ala	Asn	His	Asp	Ala	Leu	Tyr	Arg	Trp	
202		430					435				440						
204	atc	aaa	tct	gtc	gat	cct	tcc	cgc	ccg	gtg	cag	tat	gaa	ggc	ggc	gga	2836
205	Ile	Lys	Ser	Val	Asp	Pro	Ser	Arg	Pro	Val	Gln	Tyr	Glu	Gly	Gly	Gly	
206	445					450				455				460			
208	gcc	gac	acc	acg	gcc	acc	gat	att	att	tgc	ccg	atg	tac	gcg	cgc	gtg	2884
209	Ala	Asp	Thr	Thr	Ala	Thr	Asp	Ile	Ile	Cys	Pro	Met	Tyr	Ala	Arg	Val	
210				465					470					475			
212	gat	gaa	gac	cag	ccc	ttc	ccg	gct	gtg	ccg	aaa	tgg	tcc	atc	aaa	aaa	2932

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213	Asp	Glu	Asp	Gln	Pro	Phe	Pro	Ala	Val	Pro	Lys	Trp	Ser	Ile	Lys	Lys	
214				480					485					490			
216	tgg	ctt	tcg	cta	cct	gga	gag	acg	cgc	ccg	ctg	atc	ctt	tgc	gaa	tac	2980
217	Trp	Leu	Ser	Leu	Pro	Gly	Glu	Thr	Arg	Pro	Leu	Ile	Leu	Cys	Glu	Tyr	
218				495					500					505			
220	gcc	cac	gcg	atg	ggt	aac	agt	ctt	ggc	ggt	ttc	gct	aaa	tac	tgg	cag	3028
221	Ala	His	Ala	Met	Gly	Asn	Ser	Leu	Gly	Gly	Phe	Ala	Lys	Tyr	Trp	Gln	
222		510						515					520				
224	gcg	ttt	cgt	cag	tat	ccc	cgt	tta	cag	ggc	ggc	ttc	gtc	tgg	gac	tgg	3076
225	Ala	Phe	Arg	Gln	Tyr	Pro	Arg	Leu	Gln	Gly	Gly	Phe	Val	Trp	Asp	Trp	
226	525					530					535					540	
228	gtg	gat	cag	tcg	ctg	att	aaa	tat	gat	gaa	aac	ggc	aac	ccg	tgg	tcg	3124
229	Val	Asp	Gln	Ser	Leu	Ile	Lys	Tyr	Asp	Glu	Asn	Gly	Asn	Pro	Trp	Ser	
230					545					550					555		
232	gct	tac	ggc	ggt	gat	ttt	ggc	gat	acg	ccg	aac	gat	cgc	cag	ttc	tgt	3172
233	Ala	Tyr	Gly	Gly	Asp	Phe	Gly	Asp	Thr	Pro	Asn	Asp	Arg	Gln	Phe	Cys	
234				560					565					570			
236	atg	aac	ggt	ctg	gtc	ttt	gcc	gac	cgc	acg	ccg	cat	cca	gcg	ctg	acg	3220
237	Met	Asn	Gly	Leu	Val	Phe	Ala	Asp	Arg	Thr	Pro	His	Pro	Ala	Leu	Thr	
238			575					580						585			
240	gaa	gca	aaa	cac	cag	cag	cag	ttt	ttc	cag	ttc	cgt	tta	tcc	ggg	caa	3268
241	Glu	Ala	Lys	His	Gln	Gln	Gln	Phe	Phe	Gln	Phe	Arg	Leu	Ser	Gly	Gln	
242		590					595					600					
245	acc	atc	gaa	gtg	acc	agc	gaa	tac	ctg	ttc	cgt	cat	agc	gat	aac	gag	3316
246	Thr	Ile	Glu	Val	Thr	Ser	Glu	Tyr	Leu	Phe	Arg	His	Ser	Asp	Asn	Glu	
247	605					610					615					620	
249	ctc	ctg	cac	tgg	atg	gtg	gcg	ctg	gat	ggt	aag	ccg	ctg	gca	agc	ggt	3364
250	Leu	Leu	His	Trp	Met	Val	Ala	Leu	Asp	Gly	Lys	Pro	Leu	Ala	Ser	Gly	
251					625					630					635		
253	gaa	gtg	cct	ctg	gat	gtc	gct	cca	caa	ggt	aaa	cag	ttg	att	gaa	ctg	3412
254	Glu	Val	Pro	Leu	Asp	Val	Ala	Pro	Gln	Gly	Lys	Gln	Leu	Ile	Glu	Leu	
255				640					645					650			
257	cct	gaa	cta	ccg	cag	ccg	gag	agc	gcc	ggg	caa	ctc	tgg	ctc	aca	gta	3460
258	Pro	Glu	Leu	Pro	Gln	Pro	Glu	Ser	Ala	Gly	Gln	Leu	Trp	Leu	Thr	Val	
259			655					660						665			
261	cgc	gta	gtg	caa	ccg	aac	gcg	acc	gca	tgg	tca	gaa	gcc	ggg	cac	atc	3508
262	Arg	Val	Val	Gln	Pro	Asn	Ala	Thr	Ala	Trp	Ser	Glu	Ala	Gly	His	Ile	
263		670					675						680				
265	agc	gcc	tgg	cag	cag	tgg	cgt	ctg	gcg	gaa	aac	ctc	agt	gtg	acg	ctc	3556
266	Ser	Ala	Trp	Gln	Gln	Trp	Arg	Leu	Ala	Glu	Asn	Leu	Ser	Val	Thr	Leu	
267	685					690					695					700	
269	ccc	gcc	gcg	tcc	cac	gcc	atc	ccg	cat	ctg	acc	acc	agc	gaa	atg	gat	3604
270	Pro	Ala	Ala	Ser	His	Ala	Ile	Pro	His	Leu	Thr	Thr	Ser	Glu	Met	Asp	
271				705						710					715		
273	ttt	tgc	atc	gag	ctg	ggt	aat	aag	cgt	tgg	caa	ttt	aac	cgc	cag	tca	3652
274	Phe	Cys	Ile	Glu	Leu	Gly	Asn	Lys	Arg	Trp	Gln	Phe	Asn	Arg	Gln	Ser	
275				720					725					730			
277	ggc	ttt	ctt	tca	cag	atg	tgg	att	ggc	gat	aaa	aaa	caa	ctg	ctg	acg	3700
278	Gly	Phe	Leu	Ser	Gln	Met	Trp	Ile	Gly	Asp	Lys	Lys	Gln	Leu	Leu	Thr	

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281	ccg ctg cgc gat cag ttc acc cgt gca ccg ctg gat aac gac att ggc			
282	Pro Leu Arg Asp Gln Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly			
283	750	755	760	3796
285	gta agt gaa gcg acc cgc att gac cct aac gcc tgg gtc gaa cgc tgg			
286	Val Ser Glu Ala Thr Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp			
287	765	770	775	3844
289	aag gcg gcg ggc cat tac cag gcc gaa gca gcg ttg ttg cag tgc acg			
290	Lys Ala Ala Gly His Tyr Gln Ala Glu Ala Leu Leu Gln Cys Thr			
291	785	790	795	3892
292	gca gat aca ctt gct gat gcg gtg ctg att acg acc gct cac gcg tgg			
293	Ala Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp			
294	800	805	810	3940
296	cag cat cag ggg aaa acc tta ttt atc agc cgg aaa acc tac cgg att			
297	Gln His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile			
298	815	820	825	3988
300	gat ggt agt ggt caa atg gcg att acc gtt gat gtt gaa gtg gcg agc			
301	Asp Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val Ala Ser			
302	830	835	840	4036
306	gat aca ccg cat ccg gcg cgg att ggc ctg aac tgc cag ctg gcg cag			
307	Asp Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln			
308	845	850	855	4084
310	gta gca gag cgg gta aac tgg ctc gga tta ggg ccg caa gaa aac tat			
311	Val Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr			
312	865	870	875	4132
314	ccc gac cgc ctt act gcc gcc tgt ttt gac cgc tgg gat ctg cca ttg			
315	Pro Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu			
316	880	885	890	4180
318	tca gac atg tat acc ccg tac gtc ttc ccg agc gaa aac ggt ctg cgc			
319	Ser Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg			
320	895	900	905	4228
322	tgc ggg acg cgc gaa ttg aat tat ggc cca cac cag tgg cgc ggc gac			
323	Cys Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp			
324	910	915	920	4276
326	ttc cag ttc aac atc agc cgc tac agt caa cag caa ctg atg gaa acc			
327	Phe Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr			
328	925	930	935	4324
330	agc cat cgc cat ctg ctg cac gcg gaa gaa ggc aca tgg ctg aat atc			
331	Ser His Arg His Leu Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile			
332	945	950	955	4372
334	gac ggt ttc cat atg ggg att ggt ggc gac gac tcc tgg agc ccg tca			
335	Asp Gly Phe His Met Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser			
336	960	965	970	4420
338	gta tgc gcg gaa ttc cag ctg agc gcc ggt cgc tac cat tac cag ttg			
339	Val Ser Ala Glu Phe Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu			
340	975	980	985	4468
342	gtc tgg tgt caa aaa aga tct gac tat aaa gat gag gac ctc gac cat			
343	Val Trp Cys Gln Lys Arg Ser Asp Tyr Lys Asp Glu Asp Leu Asp His			
344	990	995	1000	

VERIFICATION SUMMARY

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L:2112 M:283 W: Missing Blank Line separator, <220> field identifier